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OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 18:56:08 ; Search time 893 Seconds
(without alignments)
10481.989 Million cell updates/sec

Title: US-09-727-628-3

Perfect score: 2069
Sequence: 1 tttagatttttttcaattc.....gggaattaaggaaccattgg 2069

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2937390 seqs, 2262062796 residues

Total number of hits satisfying chosen parameters: 5874780

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/prodata/1/pubpna/US05_NEW_PUB.seq:
4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:
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10: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:
14: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:
15: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:
16: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:
17: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:
18: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:
19: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2069	100.0	2069	9	US-09-727-628-3
2	187.8	9.1	1971	13	Sequence 26983, A
3	123	5.9	1912	13	Sequence 8483, Ap
4	120	5.8	1914	13	Sequence 5612, Ap
5	119	5.8	1879	13	Sequence 5704, Ap
6	119	5.8	1959	9	US-09-727-628-1
7	118.8	5.7	2155	13	Sequence 25858, A
8	105.2	5.1	753	15	US-10-425-114-25858
9	82.6	4.0	280	9	US-10-307-723-43
10	68.8	3.0	6881	15	US-09-294-0938-601
11	62.8	3.0	6881	15	US-10-311-455-1354
12	58.8	2.8	3673778	15	US-10-240-453-124
13	53	2.6	5362	15	US-10-312-841-1
14	52.2	2.5	19380	13	US-10-240-453-287
					Sequence 390, App

ALIGNMENTS

RESULT 1

US-09-727-628-3
; Sequence 3, Application US/09727628
; Patent No. US20020068359A1
; GENERAL INFORMATION:
; APPLICANT: Armstrong, Katherine
; APPLICANT: Hey, Timothy D
; APPLICANT: Folkerts, Otto
; APPLICANT: Smith, Kelley A
; APPLICANT: Hopkins, Nicole L
; TITLE OF INVENTION: MAIZE MIP SYNTHASE PROMOTER
; FILE REFERENCE: 50597
; CURRENT APPLICATION NUMBER: US/09/727,628
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/168,612
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2069
; TYPE: DNA
; ORGANISM: Zea mays
US-09-727-628-3

Query Match 100.0%; Score 2069; DB 9; Length 2069;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2069; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTAGATTTTTTCAATTCACCCGAGTAATTCGATCCATCACAATCTTAAAAATCAGGAG 60
Db 1 TCTAGATTTTTTCAATTCACCCGAGTAATTCGATCCATCACAATCTTAAAAATCAGGAG 60
QY 61 AAATTATATGCGCATTTATATAGAACCACTAAATAAATGTCGTTGTTATTGAAAAAAA 120
Db 61 AAATTATATGCGCATTTATATAGAACCACTAAATAAATGTCGTTGTTATTGAAAAAAA 120
QY 121 ACCTATTATACAAAAACATCTGCCAAGAATACAAATCTTTTATATACACAACTTATATGTGA 180

Sequence 1492, Ap
Sequence 44, Appl
Sequence 1594, Ap
Sequence 2, Appl1
Sequence 1429, Ap
Sequence 515, App
Sequence 175, App
Sequence 1795, App
Sequence 292, App
Sequence 131, App
Sequence 21, Appl
Sequence 659, App
Sequence 10, Appl
Sequence 29, Appl
Sequence 2, Appl1
Sequence 53, Appl
Sequence 618, App
Sequence 146, App
Sequence 1, Appl1
Sequence 7, Appl1
Sequence 3, Appl1
Sequence 513, App
Sequence 178, App
Sequence 36, Appl
Sequence 1310, Ap
Sequence 108, App
Sequence 308, App
Sequence 6384, Ap
Sequence 12661, A

51 2.5 5520 15 US-10-311-455-1492
50.2 2.4 5891 13 US-10-221-613-44
49.6 2.4 6254 15 US-10-311-455-1594
49.6 2.4 3673778 15 US-10-312-841-2
49.4 2.4 5488 15 US-10-311-455-1429
49.4 2.4 11790 15 US-10-311-455-515
49 2.4 23683 15 US-10-240-485-175
48.8 2.4 6113 15 US-10-311-455-1795
48.8 2.4 96588 12 US-09-997-722-292
48.4 2.3 8170 15 US-10-240-453-131
48.4 2.3 16173 15 US-10-240-485-21
48 2.3 8962 15 US-10-311-455-659
47.8 2.3 20598 13 US-10-139-667-10
47.4 2.3 1064 9 US-09-804-682-29
47.4 2.3 1069 15 US-10-389-301-2
47.4 2.3 1069 15 US-10-388-931-2
47.4 2.3 1623 13 US-10-312-352-53
47.4 2.3 1648 16 US-10-291-265-618
47.4 2.3 1651 16 US-10-291-265-146
47.4 2.3 1702 15 US-10-240-535-1
47.4 2.3 1824 16 US-10-351-161A-7
47.4 2.3 2013 15 US-10-389-301-3
47.4 2.3 2013 15 US-10-388-931-3
47.4 2.3 61020 13 US-10-221-714A-513
47.4 2.3 6271 13 US-10-221-714A-178
47.2 2.3 6271 15 US-10-172-086-36
47.2 2.3 6271 15 US-10-311-455-1310
47.2 2.3 17534 17 US-10-257-166-108
47 2.3 6099 13 US-10-221-613-308
46.8 2.3 664 10 US-09-814-353-6384
46.8 2.3 664 10 US-09-814-353-12661

; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26983
; LENGTH: 1971
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4701-002-D6_FLI
US-10-425-114-26983

Query Match
Best Local Similarity 9.1%; Score 187.8; DB 13; Length 1971;
Matches 209; Conservative 0; Mismatches 7; Indels 7; Gaps 1;

QY 1848 GTGGGTCCATTCTCTCAATTTGGCAGTGGCGGCTCGAACCCCTCTATAATCCCCCA 1907
DB 1 GTGGGTCCATTCTCTCAATTTGGCAGTGGCGGCTCGAACCCCTCTATAATCCCCCA 60

QY 1908 CCCGAGACACCTTCCCGACACACAGCCCA-----ACAAAGAGAGCGCGCGCC 1960
DB 61 CCCGAGACACCTTCCCGACACACAGCGTCCACAGCCCAACAAAGGAGCGCGCGCC 120

QY 1961 CTTCTTCTCTCTCTCCCACTTCTCTCGCGCGGCTCGGTACCTCGCTCGCATTCGGT 2020
DB 121 CTTCTTCTCTCTCTCCCACTTCTCTCGCGCGGCTCGGTACCTCGCTCGCATTCGGT 180

QY 2021 TCAGCAGGGAGCGGCGAGTGAAGAGGAGGGAATTAAGGCA 2063
DB 181 TCAGCAGGGAGCGGCGAGTGAAGAGGAGGGAATTAAGGCA 223

RESULT 3
US-10-425-114-8483
; Sequence 8483, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 8483
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700804383_FLI
US-10-425-114-8483

Query Match
Best Local Similarity 5.9%; Score 123; DB 13; Length 1912;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1941 CAACAGGAGCGGGCGGCGGCGGCTCTCTCTCCCACTTCTCTCGCGGCGGCTCGCT 2000
DB 1 CAACAGGAGCGGGCGGCGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60

QY 2001 TACTCGCTCGCATTCGGTTTCAGCAGGGAGCGGCGGAGTGAAGAGGAGGGAATTAAG 2060
DB 61 TACTCGCTCGCATTCGGTTTCAGCAGGGAGCGGCGGAGTGAAGAGGAGGGAATTAAG 120

QY 2061 CAA 2063
DB 121 CAA 123

RESULT 4
US-10-425-114-5612
; Sequence 5612, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5612
; LENGTH: 1914
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700466493_FLI
US-10-425-114-5612

Query Match
Best Local Similarity 5.8%; Score 120; DB 13; Length 1914;
Matches 132; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1930 ACAGAGCCCAACAAAGAGCGCGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1989
DB 1 ACAGAGCCCAACA--AAGAGCGCGGCGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 58

QY 1990 CGGCGCTCGCTTACCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 2049
DB 59 CGGCGCTCGCTTACCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 118

QY 2050 GGAATTAAGGCAA 2063
DB 119 GGAATTAAGGCAA 132

RESULT 5
US-10-425-114-5704
; Sequence 5704, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5704
; LENGTH: 1879
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700470105_FLI
US-10-425-114-5704

Query Match
Best Local Similarity 5.8%; Score 119; DB 13; Length 1879;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1945 AAGAGCGCGGCGGCGGCT 2004

[illegible]

1759	QY	AGTTCGGCGCTTCGGGCAATCCGCGGCGCGCGTCCGCTCAAAATCGCAT-----CCTACCG	1871	DB	AGTTCGGCGCATCCGCGCAATCCCGCGGCGCGCGTTCGATTCGATCGTACCTCGACG	126
67	DB	AGTTCGGCGCATCCGCGCAATCCCGCGGCGCGCGTTCGATTCGATCGTACCTCGACG	1814	QY	CGGCTAGAGCTCTCTCTTCC--TCGCTCGATCCGGTGGGGTCCATTTCTCTCAATTGT	1871
127	DB	CGGCTACGAGCTCGCTCCTCCGCTCCGCTCCGCTCCGATCCCGTGGGGTCCGTTCTTTTCAGCGC	186			
1872	QY	GGCAGTGGCGGTC-----TCGAACCCCTCTATAAATCCGCCACCCGCCG	1913			
187	DB	GGCTCGCTGGCGCCTCGTGGCAGTGACGTCGAACCCCTCTATAATCCGTCGCCCGCA	246			
1914	QY	ACACCTTTCGGGACACACAGGCCAA--CAACAAGGAGCGCGGCGGCCCTCTCTTCCTT	1971			
247	DB	GCACCTTCTCGATCACACACCCCAAGCAGCCACAGACCTCTCTTCGGCTTCCTC	306			
1972	QY	CCTCCACTTCTCTCGCGCGGCTCGCTTACCTCGCTCGCATTCGGTTCGAGCAGGGG	2031			
307	DB	CTCTCACTCTCGCTCGCTCGCTCGC-TACCTCGCTTCGCATTCATTCCGAGGAGC	365			
2032	QY	AGCGGCAGTG	2041			
366	DB	GGTGAGAGGG	375			

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: Sequence 43, Application US/10307723
: Publication No. US20030131375A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Conner, Timothy W
:
: APPLICANT: Tzafirir, Iris
:
: TITLE OF INVENTION: Plant Regulatory Sequences for Selective Control of Gene
:
: FILE REFERENCE: 06009, 0019, DVSU01 (RENN:019--1)
:
: CURRENT APPLICATION NUMBER: US/10/307,723
:
: CURRENT FILING DATE: 2002-12-02
:
: PRIOR APPLICATION NUMBER: US/09/651,169
:
: PRIOR FILING DATE: 2000-08-30
:

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; SEQ ID NO 43
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Zea Mays
US-10-307-23-43

Query Match          5.1%; Score 105.2; DB 15; Length 753;
Beat Local Similarity 69.4%; Pred. No. 9.1e-16;
Matches 247; Conservative 0; Mismatches 68; Indels 41; Gaps 6

QY      1636  CTGCGAGCGCGGCGCTCCCATTTTCGCTCCCTCCTACTCTCTATGCTGGGTCCAGC 1755
Db      410  CGGCGCGCAGCGGAGTCTCTCCATTTCGCTCCCTCC-----CTCCTCCGCTGGGTGAGC 464

QY      1756  AAAAGTTTCGGGCTTCCGGCAATCCGGCGGCGCCGCTGGGTCAAATCGCAT-----180
Db      465  AAAAGTTTCGGCCATCCGGCAATCCCCCGCACCCGGGTTCAAACGATCTTTCTGA 524

QY      1808  -CTACCGGGGTGAGAAGTCTCTTTCC--TCCTCCGATCCGGTGGGGTCCATTTCCCT 1866
Db      525  CCTGACGGGGCTACGACGTGCTCTCCGGTCCCTTCGATCCGGTGGGGTCGGTTCTTT 584

QY      1865  CAATTGTGCAGTGCCCGTC-----TCGAACCTCTATATAATCCCCC 1900

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QY      1907 ACCCGGACACCCTTCCCGGCACCAAGGCCAACAAACAAGGAGCGGGCGGCCCTCCT 1966
Db      645 GCGCCGAGCACCCCTTCTTCGTATCACAAACC-----CAAAGCAGCCACAGCAGCCTCCT 698
QY      1967 TCCTCTCCCACTTCTCTCGCGGGCGCTCGCTTAACCTCGCCCTCGCATTTCCGTTTC 2022
Db      699 TCTCTCTCACTCTCGCTCGCGTGCGCTGCG-TACCTCGCTTCGATTCCATTTC 753

RESULT 9
US-09-294-093B-601
; Sequence 601, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 601
; LENGTH: 280
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700343034H1
; NAME/KEY: unsure
; LOCATION: 5, 9, 13, 37, 39, 42, 46, 61, 66, 88, 196, 259, 266
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-601

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	Query Match	4.0%;	Score 82.6;	DB 9;	Length 280;
	Best Local Similarity	82.2%;	Pred. No. 2.4e-10;		
	Matches 88;	Conservative 0;	Mismatches 19;	Indels 0;	Gaps 0;
Qy	1948	GAGCGCGGCGCCCTCTCTTCTCTCCACATTTCTCTCGCGCGCGCGCTCGCTTACTCG			2007
Db	1	GAGNCGNGGNCCTCATTCCTTCTCTCCACATTTCTNTNGNCNTGNGCTCGCTTACTCG			60
Qy	2008	CCTCGCATTCGTTTCGACGAGGGGAGCGGCAGTGAAGAGGGAGAA			2054
Db	61	NTTCGNATTTGGGCTTCGACGAGGGGAGNGCGCGTGAAGAGGAAGGA			107

RESULT 10
US-10-311-455-1354/c
; Sequence 1354, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENROCK, Christian
; APPLICANT: BESLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311.455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1354
; LENGTH: 6881

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1354

Query Match      3.0%; Score 62.8; DB 15; Length 6881;
Best Local Similarity 44.2%; Pred. No. 0.0002;
Matches 349; Conservative

QY      16  AATTCACCCGGAGTAAATATCCAAATCACAAATCTAAAAATCAGAGAGAAATATATATGGCCAT 75
      |||
Db      6837  AATTATCTCTTTACCTAATTAATAATTAATTTCTTAATAAATAATATTAATAATTA 6778

QY      76  ATTATAGAGCAACTAAATPAAAAATGCGGTGTATTGAAAAAATAAACCTATTATTATACAA 135
      |||
Db      6777  TTTAAAAACAATAATTTTAAAAAATAATTAATAAATATCAATATTAACAAAAATAAAAA 6718

QY      136  ACATCTGCCAAGNATACAAATCTTTTATACAGAACTTATATGAGCACTTCTTTCTCTCTTG 195
      |||
Db      6717  ATTTTTATTATACAAATACTTTTTHAATAACATAAAATTTTACCATATATTCAAATTTA 6658

QY      196  TAACTCTTTATTAATAAAACATTTTGGCTATTAAATAATATGGCAACTAAGTTAG -CACCA 253
      |||
Db      6657  TAAATTCATTTTACAAAAAATACTTCCAAAAAATAATACTATTTTCTTCTACACAT 6598

QY      254  CTGTAAATTAGATTTTCTCTGGAAACAATTTCTCTGACTTAAGAAGCTATTGGAGTGTCTTT 313
      |||
Db      6597  CTTTACACATTTCTTAATCTAAATCTTATCAAAAAAATAAATATTTTAAAAATATTT 6538

QY      314  TTGCCAAACAGPAGAAAAATGGAACCGCTCTTTAAAAAACCAATCTTCACATCCGCTGGTG 373
      |||
Db      6537  ATATTAAATAATTTTAAATAAAATCGATTAATAAATACTAATAATAAAATCTACAACATATC 6478

QY      374  CTGAATAAABACTGAAACCAATTAGCTTTTATAGCTCTCGCTCTCTGTAGTAGTGTAT 433
      |||
Db      6477  CAAATATATAAATATTAAACAAACAATTAATCTTCTTTAACCATCTTATAAAAAAATA 6418

QY      434  AAAATCATTTTACCAATTAACCTTTTAAATAAATGAGTACGTAGTAGTTTCATCAGTAGAATC 493
      |||
Db      6417  CAAACAATTTAATCAATTTACTATCTCAATACAAATAAATAAATAACAAAAACAAACAAT 6358

QY      494  TCACGGAGCTAAACAAAAAAGTGTCTTCTACTGATATAAAGACGAGATGATGTATGACCG 553
      |||
Db      6357  AAAACACCTTCAAAAAATAAANAATAATTTATTTTCAAAAAACAATTTTTCAAAA 6298

QY      554  TGACCGGTGAGCT - AAAGTCCAAAAAATAAACTGCTCCAATATACGACAAACAAGT 611
      |||
Db      6297  TAAAAATTTATTTCTTATATCAATAATATAAATCTACTACCCCAATAACACAAATACTATA 6238

QY      612  TGTATTGTATGGCTAAATTAACGACACTGACGACACAGTATATTATTCTCTCTCCAT 671
      |||
Db      6237  AATAAATTTATCAAAATTAATTTAAATAATATATCTTATAATACTAATAATAAATTTCTA 6178

QY      672  TATCACAGGATGAACGTGTAATAAATTTGTATGTTAAACATTTGTAGTAAATATTTGCTAG 731
      |||
Db      6177  CAAAAATAATTTTATTAATAAATACTTTAAAAATTTACCTCAACTCGTAAACATACAAATA 6118

QY      732  CATTACGCTCTACGGAATTTTATGAAAAAATGTAGTATTTGTTTATATAATTTTAAATAAA 791
      |||
Db      6117  TATCTATTTTCACTATCTACATTTAANAATCTTATCTTAATTCATTTAAAAAATAAT 6058

QY      792  ACTGTAAATC 801
      |||
Db      6057  AAAATAAATC 6048

RESULT 11
US-10-240-453-124/c
; Sequence 124, Application US/10240453
; Publication No. US20030148326A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander

```

RESULT 11
US-10-240-453-124/c
; Sequence 124, Application US/10240453
; Publication No. US20030148326A1
; GENERAL INFORMATION:
; APPLICANT: OLEPK, Alexander

APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Transcription
TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated
TITLE OF INVENTION: With DNA Transcription
FILE REFERENCE: 5013.1009
CURRENT APPLICATION NUMBER: US/10/240,453
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/03973
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 350
SEQ ID NO 124
LENGTH: 6881
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-453-124

Query Match 3.0%; Score 62.8; DB 15; Length 6881;
Best Local Similarity 44.2%; Pred. No. 0.0002;
Matches 349; Conservative 0; Mismatches 437; Indels 4; Gaps 2;

* QY 16 AATCCACCCGAGTAATCCAAATCACAATCTAAATCAGGAGAAATATATGCGCAT 75
Db 6837 AATTATCTCTTTACCTAATAAAATAATCTTAAATAAAAAATAATTAATAATTA 6778

QY 76 ATTATAGAGCACTAAATAAATGCGTGTATGAAATAAAACCTATTATAACA 135
Db 6777 TTTAAAAACAATATTAAAAATAATTAATAATCAAAATTAACAAAAATAAAA 6718

QY 136 ACATCTGCCAAGTAACAATCTTTATACACAACCTTATATGAGTCTCTTTCTCTTG 195
Db 6717 ATTATATATACAAATATCTTTTAAATAACATAAAATTTTACCATAATTCATTTA 6658

QY 196 TAATCTTATTAATAAAACATTTTGGCTATTAATTAATGGAACCTAGTTAG--CACCA 253
Db 6657 TAATTTCAATTTTCAAAAAAATCTTTCCAAAAAATAAATCTATTTTCTTACACAT 6598

QY 254 CTGTAAATAGATTTGTCTGCAACAATTTCTCTGACTAAGAGCTATTTGGACTGTCTT 313
Db 6597 CTTTACACATTTCTAATCTAATCTAATCTAATCAAAAAAATAATTTTAAATAATTT 6538

QY 314 TTGCCAAACAGTAGAATAATGGAACCGCTCCTTAAAAAACCATCTTCACATCGCTGGTG 373
Db 6537 ATATTAAATTAATTTTAAATAAATCGACTAAAAAATACTAAATAAAAACTCAACTATC 6478

QY 374 CTGTAATAAACTGAACATAGCTTTTATAGCTCTGCTCTCTGCTAGTATGTGTTAT 433
Db 6477 CAATATAAATAATTAACAACAATTAATTAATTTCTTTAACCATCTTATTAATAAAAA 6418

QY 434 AAATCAATTTTACCAATTTTATTAATAATCTGATGAGTTTCAATGAGTACCTAC 493
Db 6417 CAACAATTTTAACTACTCTCTCAATCAATAAATAAATAAACAACAACAACAAT 6358

QY 494 TCACGGAGCTAAACAATAAAGTGTCTTACTGATTAAGACGAGATGATGATGATGATG 553
Db 6357 AAAAAACCTTTCAAAAAATAAACTAAATTTTATTTTCAAAACCAATTTTTCACAA 6298

QY 554 TGACCGTGAGCT--AAAGTCCAAAAAATAAACTGCTCCCAATAACGACAAAAACAAGT 611
Db 6297 TAAAAAATTTATTTCTTATATCAATAATAATTAATTAATTAATTAATTAATTAATTA 6238

QY 612 TGTATTGTAGGCTTAATTTACAGCACACTGACACACGATATATTTCTCTCTCCAT 671

Db 6237 AATAAATTTATCCAAATAAATTTTAAATATATATCTTATATACTAAAAATAATTTCTA 6178
QY 672 TATCAGCAGATGTAAGTGTAAATAATTTTGTATGTTAAACATTTGTAGTAATAATTGCTAG 731
Db 6177 CAATAAATTTTATTAATAAAAAATCTTAAATTTACTCACTCGTAATAACATTAACAATA 6118
QY 732 CATTTACGCTACGGAATTTATTTGAAAAAATCTAGTATTGTTTTATATAATTTTAAATA 791
Db 6117 TATCTATTTCACTATATCTACATTAATAATCTTCTTAAATTCATTTAAAAATAATAAT 6058
QY 792 ACTGTAAATC 801
Db 6057 AAAATAAATC 6048

RESULT 12
US-10-312-841-1/c
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: 801/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1

Query Match 2.8%; Score 58.8; DB 15; Length 3673778;
Best Local Similarity 44.2%; Pred. No. 0.13;
Matches 329; Conservative 0; Mismatches 412; Indels 3; Gaps 2;

QY 49 AAAAATCAGGAGAAATATATATGCGCATATTTATAGAGCAACTAAATAAATGTGCGTGT 108
Db 1714131 AAATATATAAATAATATATAAATAATATAAATAATATAAATAATATAAATAATATA 1714072

QY 109 ATTGAAAAAARACCTATTTATACAAACATCTGCCAAGAAATCAATCTTTTATACACA 168
Db 1714071 AATATATATAAATAATATATAAATAATATAAATAATATAAATAATATAAATAATATA 1714012

QY 169 ACTTATATGTGAGTTCTTTTCTCTGTAACCTCTTATTAATAAACAATTTTGGCTATT 228
Db 1714011 ATATATATAAATAATATAAATAATATAAATAATATAAATAATATAAATAATATA 1713952

QY 229 AATAATGCGCAACTAAGTTAGCACCACTGTAAATAGATTTTGTCTGGAACAATTTCTCTGA 288
Db 1713951 AATATATAAATAATATAAATAATATAAATAATATAAATAATATAAATAATATA 1713892

QY 289 CTAAGAAGCTATTTGGAGCTGTCTTTTGGCAACAAGTAGAAAAATGGAACCGCTCCCTAA 348
Db 1713891 ATAT-ATAATATAAATAATATAAATAATATAAATAATATAAATAATATAAATAATATA 1713833

QY 349 AAAACCATCTTCACATCGCTGGGTGCTGATTAATAAATAAATAAATAAATAAATAAATAA 408
Db 1713832 AAAATATATAAATAATATAAATAATATAAATAATATAAATAATATAAATAATATA 1713773

QY 409 CTCGCTCTCTGCTAGTGTCTTATAAATCATTTTACCAATTTACCTTTTAAATAAATCTG 468
Db 1713772 AAAATATATAAATAATATAAATAATATAAATAATATAAATAATATAAATAATATA 1713713

QY 469 TACGTAAGTTTCATCAGTAGAAGTCTCTACGAGCTAAACCAAAAAAGTTGTTCTACTGA 528
Db 1713712 ATATATAATATAAATAATATAAATAATATAAATAATATAAATAATATAAATAATATA 1713653

QY 529 TAAAGCAGAGATGATGATGACCGGTGAGCTAAAGTCCAAAAAAGTCTCT 588
Db 1713652 ATATATAAATATATATAAATATATAAATATATAAATATATAAATATATAA 1713593
QY 589 CCACATACGACAAACAAAGTTCTATGTTGATGCGCTAAATACAGCACCTGACACCA 648
Db 1713592 ATATATAAATATATAAATATATAAATATATAAATATATAAATATATAAATATA 1713533
QY 649 CACGATATATATCTCTCTCCATATACAGGATGTAAGTGTAAAAATTTTGTATGTTAA 708
Db 1713532 TATATAAATATATATAAATATATAAATATATAAATATATAAATATATAA 1713475
QY 709 ACATTTGTAGTAATATCTCTAGCATTTACGCTACGGATTTATGAAAAATCTAGTA 768
Db 1713474 ATATATAAATATATAAATATATAAATATATAAATATATAAATATATAAATATA 1713415
QY 769 TTGTTTATATATATTTTATAA 792
Db 1713414 ATATATAAATATATAA 1713391

RESULT 13
US-10-240-453-287/c
; Sequence 287, Application US/10240453
; Publication No. US20030148326A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
; TITLE OF INVENTION: Transcription
; TITLE OF INVENTION: By Means of Assessing the Methylation Status of Genes Associated
; TITLE OF INVENTION: With DNA Transcription
; FILE REFERENCE: 5013.1009
; CURRENT APPLICATION NUMBER: US/10/240,453
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03973
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 287
; LENGTH: 5362
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-453-287

Query Match 2.8%; Score 53; DB 15; Length 5362;
Best Local Similarity 42.8%; Pred. No. 0.05;
Matches 326; Conservative 0; Mismatches 430; Indels 5; Gaps 1;
QY 49 AAAAAATCAGGAGAAATATATGCGCATATATAGAAGCAACTAAATAAAAATGCGGTGT 108
Db 4846 AATACCGGAAATATTTCTATATACCATCTTAACAAATCGCAAACTTAATCATCATCTT 4787
QY 109 ATTGAAAAAACCCTATTTATTAACAAACATCTGCCAAGATACATTTCTTTTATACACA 168
Db 4786 AAAAAATACAACTACAAAAAACCGTAACCTCTCTTAACCGGCAAACTACTATAAAT 4727
QY 169 ACTTATATGAGTCTCTTTCTCTGTAACCTCTTATTAATAAACAATTTTGGCTATTA 228
Db 4726 ACTATACTATTAACAATAAACCGGATTAATTTCTTATTAATAAACAATTTTGTAGTCT 4667
QY 229 AATAATGGCAACTAAGTTAGCACCACCTGTAATTTGTTCTGGAAACAATTTCTCTGA 288

RESULT 14

US-10-221-613-390/c
; Sequence 390, Application US/10221613
; Publication No. US20040029123A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle
; FILE REFERENCE: 5013.1004
; CURRENT APPLICATION NUMBER: US/10/221,613
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: PCT/EP01/02945
; DE 10013847.00
; DE 10019058.8
; DE 10019173.8
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-03-15
; 2000-03-15
; 2000-04-06
; 2000-04-07
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 428
; SEQ ID NO 390
; LENGTH: 19380
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-613-390

Db 4666 CTTTCATCCCAAACTAAAAATATATATAAAAAACCCTTTCTTTCAAAATCCCAAC 4607
QY 289 CTAAGAGCTATTTGACGTGCTCTTTTGGCAACAAGTAGAAAAATGGAACCGCTCTTTAA 348
Db 4606 CTATACCTTATCTTTAAACAACGTAATATATAAATAAAGCTTTTAAAAAATAATTTAA 4547
QY 349 AAAACCAATCTCAGATCGCTGGGTGCTGAATAAACTGAA-----AACATTAGCTTTTA 403
Db 4546 TCACATAAAAAACATAAAAAACTACTTCTAAACCTCAGACCAAAATTTCTTTCAA 4487
QY 404 TAGCTCTCGCTCTCTCTGCTAGTATGTTTATAAATCAATTTTACCAATTAACCTTTTAAAT 463
Db 4486 AAACCAACAACTTAATTAACATACGATTATAAACAATAATCAATTTTAAAAAT 4427
QY 464 AACTGTACGTAGTTTCATCAGTAGAAGTCTACGAGGTAAACAAACAAAGTTTGTCT 523
Db 4426 ATAAACTCCCTACCTATATATCCCACTACTAAAAAACTTAAAAACAAACAAATCGCTTAA 4367
QY 524 ACTGATAAAAGCAGAGATGATGATGACCGGTGAGCTAAAGTCCAAAAAAGTCTCA 583
Db 4366 ACCGAAAAACGAAACTTAATTAACGTAATAAATAACACTATATATCCCACTAC 4307
QY 584 CTGCTCCACAATTAACGACAAACAAGTTGTTATGTCCTTAATTTAGCCTTAATTAACGACACTGA 643
Db 4306 CTAATAAACTAAACAAAAAATCAATTAACCCGAAAAACGAAAAATTAACGAAACCGA 4247
QY 644 CACCACAGGTATATTCTCTCTCCATATATCAGGATGTAACCTGTAAATAATTTGTAT 703
Db 4246 AATCTTACCTACACTCTCCATCTAAATAACAAACGAAACTCTATCTCAAAAAA 4187
QY 704 GTTAAACATTTGTAGTAAATATTGCTAGCAATTTACGCTACGGAATTTTGAATAATG 763
Db 4186 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4127
QY 764 TAGTATTGTTTATATATATTTTAAATAAACTGTAAATCGTC 804
Db 4126 ATTCTTCTCCACATAAATACTAATAATCAATTTTAAAAATC 4086

Query Match 2.5%; Score 52.2; DB 13; Length 19380;
Best Local Similarity 44.6%; Pred. No. 0.19;
Matches 335; Conservative 0; Mismatches 408; Indels 8; Gaps 3;
108 TATTGAAAAAAGAACTATTATTAACAACATCTGCCAGATACAAATCTTTTATACAC 167
168 AACTTATATGTGAGTCTTTTCTCTTGTGTAATCTTTTAAATAAACAATTTTGGCTATT 227
2706 ACTTCTTACACATTAAATTTTAAATTCACAAACATATATTAATATCTACTATATAAAT 2647
228 AATAATGGAACAACTAGTTAGACCACTGTATTAATAGATTTTCTGCGAACATTTCTCTG 287
2646 CTATATTACTTACTTAAATAAATACTAAATAATATTAATAAATAAATAAATACTTTCCC 2587
288 ACTAAGAGCTATTGAGCTGCTCTTTGCGCA---AACAAAGTAGAAATGGAACGCTCC 344
2586 TCATAAATAAACAACAACAACATCTACTATACACAAATATATTAATTACTACGCA 2527
345 TTAATAAACAATCTCACATCGCTGGTCTGTAATAAATCTGAAACATTAAGCTTTTAT 404
2526 TCAATAATATAACAATAAATAATAAATATATATATAAATAAATAAATACTTTAACTTATTA 2467
405 AGCTCTCGCTCTCTGTAGTATGTTTATAAATCATTTTACCAATTACCTTTTAAATA 464
2466 AATAATTTATACAAATATATAAATAAACAATCATCACTACCTATCAATAAACA 2407
465 ACTGTACGAGTTTCATCAGTAGAATCTACTACG--GAGCTAAACAATAAAGTTGTC 522
2406 AAAACAATATTTTAAATAAATAAACAACCTACGAAAAAATTAATAAATAAATAAATA 2347
523 TACTGATAAAGCAGAGATGATGATGACCGTGACCGTAAAGTCCAAATAAATAAATA 582
2346 TTACCAACAATAAATAATTTTAAATATACCTAATATTTAAATTTAAATTAATAAATAA 2287
583 ACTGCTCCACAATAAGCAGAAAAACAAGTTGATGTATGTGCGCTAAATTTACGACACTG 642
2286 GATAACAATAAATAAATACTTAAATCTACTTACAAAAATAAATAAATAAATAAATAA 2227
643 ACACCACAGCTATATTTCTCTCTCCATTCACAGGATGTAACGTAAATAAATTTTGA 702
2226 AACCTTAA--ATATCATTTTAAATTTTAAATTTTAAATTTTAAATAAATAAATAA 2170
703 TGTTAAACATTTGTAGTAAATATTTGCTAGCAATTTAGCTTACGGAATTTATGAAAAAT 762
2169 TATTAAAAATAAACAACCTTTCTAATCTATAATTTTAAATAAATAAATAAATAA 2110
763 GTAGTATTTTATATATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATA 822
2109 TAAAAATATATTAATAATTTTATAAATAAATAAATAAATAAATAAATAAATAAATA 2050
823 GAGGATAAATAGTGAATACGAATGGGAAACA 853
2049 TCTAACTAAATTTCTAAAAATAAATTTAATACA 2019

RESULT 15
US-10-311-455-1492/c
; Sequence 1492, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIERBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Methylation of Cytosine
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311.455
; PRIORITY FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1492
LENGTH: 5520
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
NAME/KEY: unsure
LOCATION: 2693, 2820
OTHER INFORMATION: n is a or g or c or t
US-10-311-455-1492
Query Match 2.5%; Score 51; DB 15; Length 5520;
Best Local Similarity 53.2%; Pred. No. 0.16;
Matches 108; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
QY 13 TTCAATTCACCCGAGTAAATATCCCAATCAATCTAAATAATCAGGAGAAATTTATATGGC 72
DB 3334 TTAATAAATAAATAAATAAATAATTCCTAATAAACAATTTTCAACAATATATTTT 3275
QY 73 CATATTATAGAGCAACTAAATAAATGTCGTTGTATTTGAAAAAACCCTTTATATA 132
DB 3274 AATATTAAACAAAAATAAATAATATCTATAAATAATATTTAAAAAACCCTTTATATCT 3215
QY 133 CAACATCTGCCAGATACAAATCTTTTATACACAACTTATATGTGAGTCTTTTCTC 192
DB 3214 TATTCTAAATAAATCTTTTAACTTTATTTTAAATAATATATTAACCTAGCAATCACAAT 3155
QY 193 TTGTAACCTTTTATTAATAAACA 215
DB 3154 ATCTCAATCTCAATAAATAAATA 3132
Search completed: May 5, 2004, 22:45:30
Job time : 908 secs

US-09-596-196-2/c
; Sequence 2, Application US/09596196
; Patent No. 6586390
; GENERAL INFORMATION:
; APPLICANT: Haley, Dana A
; APPLICANT: Boyle, Bryan J
; APPLICANT: Ho, Alice S
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Tang, Y. Tom
; APPLICANT: Tillinghast, John S
; APPLICANT: Sinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Dmanac, Radoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL
; TITLE OF INVENTION: PROTHROMBINASE-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: HYS-14
; CURRENT APPLICATION NUMBER: US/09/596,196
; CURRENT FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1069
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-596-196-2

Query Match 2.3%; Score 47.4; DB 4; Length 1069;
Best Local Similarity 46.6%; Pred. No. 0.00078;
Matches 186; Conservative 0; Mismatches 211; Indels 2; Gaps 1;

QY 48 TAAAAATCAGGAGAAATATATGCGCATATATAGCAAGCACTAAATAAATAATGCGGTG 107
Db 996 TTAATATCATTAATATTTAGGAAGCAAGTGTAGTTCACCTTGAACAAATTCATTG 937
QY 108 TATTGAAAAAACCCTATTATTAACAACAACATCTGCCAAGATACATTTCTTTATACAC 167
Db 936 TATATTGTTAATATAGTCAGAAGTAAACACATCAATAAGCCATGTTTCTTTTATAGAA 877
QY 168 AACTTATATGTGAGTCTCTTTTCTTGTAACTCTTATTAATAAACAATTTTGGCTATT 227
Db 876 TACTACAAAT--TGAAGTTTCTAATAAATCAATCAATCAATCAATCAATCAATCAAT 819
QY 228 AAATAATGGCAACTAAGTACACCACTGTAATAGATTTTGTCTGGAACAATTTCTCTG 287
Db 818 AAATTTGCGCTAATATGTTTGAACACTAAGTGAAGAAAGATAAACTTTTAAAAATCTTTAA 759
QY 288 ACTAAGAGCTATTGGAAGTCTCTTTTGGCAACAAGTAGAAAATGGAACCGCTCCTTA 347
Db 758 TATATTATCATTTGTAGAACTTGCATTACAATGTTAAATGAGATTATTTAAATATGANT 699
QY 348 AAAAACCATTTCTACATCGCTGGTGGTGAATAAATACTGAAACATTTAGCTTTTATAGC 407
Db 698 GTACATCTCTTATTTTTCATTGAACAGATTAACTCTGCAGAGTGAGTTGTTTTTGGT 639
QY 408 TCTGCTCTCTGCTAGTATGTTTATATAAATCATTTTAC 446
Db 638 CCAGTGGCCCAATTAATCCAGTTGCAAGCAATTTTCC 600

RESULT 7
US-09-596-196-3/c
; Sequence 3, Application US/09596196
; Patent No. 6586390
; GENERAL INFORMATION:
; APPLICANT: Haley, Dana A
; APPLICANT: Boyle, Bryan J
; APPLICANT: Ho, Alice S
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Tang, Y. Tom

US-09-593-995-10/c
; Sequence 10, Application US/09593995
; Patent No. 6406888
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: HELICAL CYTOKINE ZALPHA33
; FILE REFERENCE: 99-38
; CURRENT APPLICATION NUMBER: US/09/593,995
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 60/139,121
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 20598
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-593-995-10

Query Match 2.3%; Score 47.8; DB 4; Length 20598;
Best Local Similarity 49.4%; Pred. No. 0.0053; Indels 0; Gaps 0;
Matches 124; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 27 AGTAAATATCCAAATCAATCTAAATCAGGAGAAATATATGCGCATATATAGAGC 86
Db 8561 AGTTAAAAACAAAGTACAGTTTAAAAAAGTGAATCTGATGATATTTAGTGAAGA 8502
QY 87 AACTAAATAAATGCGTGTGTTGTAATGAAAAAACCCTATTATACAACATCTGCCAA 146
Db 8501 AAATGAAGATATATGCGTGTGTTGCAAAATATTTCTCAAAATGCTTAACTCTGATAA 8442
QY 147 GAATAAATCTTTTATACACAATCTATATGAGTCTTTTCTCTCTGTAAGTCTTATT 206
Db 8441 GATAATTAAGATGCTTAAAGCATACATTAATAATTAACCTGCTATTAAGTTTACTT 8382
QY 207 AATAAACAATTTTGGCTATTAATAATGGAAGTAAAGTACACCACTGTAATAGATT 266
Db 8381 AAAAAATCAATAGCAGGAGATATGGTGCATCTATCTGTAACACCACTTAATAATTA 8322
QY 267 TTGCTCTGAAC 277
Db 8321 TTACAGTAAC 8311

RESULT 6

APPLICANT: Tillinghast, John S
APPLICANT: Sinku, Ankura
APPLICANT: Liu, Chenchua
APPLICANT: Dmanac, Radole T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL
TITLE OF INVENTION: PROTHROMBINASE-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-14
CURRENT APPLICATION NUMBER: US/09/596,196
CURRENT FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 2013
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1167)
US-09-596-196-3

Query Match 2.3%; Score 47.4; DB 4; Length 2013;
Best Local Similarity 46.6%; Pred. No. 0.0013;
Matches 186; Conservative 0; Mismatches 211; Indels 2; Gaps 1;

QY 48 TAAATATCGGAGAAATATATATGCGCATATATAGAACCACTAATAAATGTCGGTTG 107
DB 1447 TTAATAATCACTAATAATTTTAGGACACAGTTGATGTCCTTGAACCAATTTTCATTG 1388

QY 108 TATTGAAAAAAACCTATTATTAACAACATCTGCCAGATACAAATCTTTTATACAC 167
DB 1387 TATATGTTAATAGTCAGAGTAAACATACATAGCCATGTTTCTTTTATAGAA 1328

QY 168 AACTATATGTCAGTTCTTTTCTCTGTTGTAACCTATATTAATAAACAATTTTGGCTATT 227
DB 1327 TACTACAAAT--TGAAGTTTCTAATTAACCTCAACATCTAATGCGCATCTACAGTT 1270

QY 228 AATATATGCACTAGTTAGCACCCTGTAATATAGATTTCTCTGGACAAATTTCTCTG 287
DB 1269 AATTTTGGCTATATGTTTGAACACTAAGTGAAGATTAACCTTTTAAATCTTTAA 1210

QY 288 ACTAAGAAGCTATTGCACTGTCCTTTTCCCAACAGTAGAATAATGGACCGCTCCTTA 347
DB 1209 TATATATCATCTTAGAAGCTTGCAATACAAATGTTAAATGAGATTATTTAAATATGGATT 1150

QY 348 AAAACCATCTCAGATCGCTGGTCTGATATAAACTGAAACATTAAGCTTTTATAGC 407
DB 1149 GTACATCTTCTAATTTTCAATGAACAGATTATCTTGCACAGGTGAGTTGTTTGGT 1090

QY 408 TCTCGCTCTGCTAGTATGTTGTATATAAATCATTTTAC 446
DB 1089 CCAGTGGCCCATGTAATCCAGTTGCAAGCAATTTTCC 1051

RESULT 8
US-09-790-988-1
Sequence 1, Application US/09790988
Patent No. 6632935
GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HAYTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 640661
TYPE: DNA
ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 2.2%; Score 44.8; DB 4; Length 640661;
Best Local Similarity 48.8%; Pred. No. 0.55;
Matches 121; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 76 ATTATAGAACCACTAATAATAATGTCGGTGTATGTGAAAAAACCCTATTATACAA 135
DB 294683 AATTTAACACCACTTTAATCTACATTCATCTCTGGGAGATAAAATATGAAGATGACAA 294742

QY 136 ACATCTGCCAAGATACAAATCTTTTATACACAACTTATATGTCAGTTCTTTTCTCTTG 195
DB 294743 ATAAAGATTTAATTCAAATGTTTAAATTAAGAAGTGAAGTTTATTTTAAAGAG 294802

QY 196 TAACTCTTATTAATAAACAATTTTGGCTATTAAATAATGCGCACTAAGTAGGACCACT 255
DB 294803 TTAATCTAAATTTTAGAAATTTTATATCAACAGTAAATTAATAAATAATTCATAA 294862

QY 256 GTAAATTAGATTTGTCGGAAACAATTTCTCTCACTAAGAAGCTATTGTCAGTCTCTTT 315
DB 294863 TAAATTTGTTTTTTTATCTTAATTTTCCGTATAGAATTTATTTTAAAGTTAATTTTC 294922

QY 316 GCCAAACA 323
DB 294923 AACATATA 294930

RESULT 9
US-10-204-708-51/c
Sequence 51, Application US/10204708
Patent No. 6677731
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 51
LENGTH: 5219
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-51

Query Match 2.1%; Score 43.6; DB 4; Length 5219;
Best Local Similarity 46.0%; Pred. No. 0.036;
Matches 148; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

QY 374 CTGAATAAACTGAAACATTAAGCTTTTATAGCTCTCGCTCTGCTAGTATGTTAT 433
DB 4298 CTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4299

QY 434 AAATCATTTTACCAATTAACCTTTTAAATAAATGTCAGTAGTTTTCATCAGTAATAC 493

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Query Match      2.0%; Score 41.2; DB 4; Length 399;
Best Local Similarity 8.1%; Pred. NO. 0.029;
Matches 25; Conservative 156; Mismatches 129; Indels 0; Gaps 0;
QY 1469 TGTGGGGGTCATGTCATCGCAACCGACAGCAATTGCTAGTGTCTGTTTTTGACA 1528
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23 WGMVTRGSKSWRAKWSNMKKRRRRRAWWKSMCMKSKSWRSWGMVTKRMKGRGA 82
1529 COTGATAGCAITTTGATTCGTTCAATTTGAACCTGTTAACTTATATATAGAGAA 1588
83 ASWAGYMSMTYTRWRYRKYRKAAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGW 142
1589 ATTAGTCCAACTCATGCTTTAATAAAGATATAAACCACATCGAATTTAAGAAATATGATA 1648
143 YWAMKSKESMRRRRRAVWYVWYVWYVWYVWYVWYVWYVWYVWYVWYVWYVWYVWY 202
1649 GCAGGTATCTATCATCTGCTCATCTGCTCATCTGCTCATCTGCTCATCTGCTCATCTG 1708
203 WMSYAGWMSWMTWRRRCASYSWSSYCWGAKWMMYKTSRWSYYSYRCKYRSRCC 262
1709 AGGCGTCCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1768
263 WMSYCWYKTYRSWYSCYVYKTSKASCCWMMCCWMMCCWMMCCWMMCCWMMCCWMMCC 322
1769 TTCGGCAAT 1778
323 RYRSCYSAK 332

RESULT 13
US-09-621-976-2813/C
Sequence 2813, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 235..399
US-09-621-976-2813

Query Match 2.0%; Score 41.2; DB 4; Length 832;
Best Local Similarity 13.4%; Pred. No. 0.049;
Matches 54; Conservative 173; Mismatches 176; Indels 1; Gaps 1;
110 TTGAAAAAAGCACTATTATATACAAACATCTCCCAAGATCAATCTTTTATACACAA 169
405 TTGCTAAAGTACAAAGATCTACCAATAATAATTATTTTGTYYWTKWTKWYWTYYT 346
170 CTTATATGTGAGTCTTTTCTCTGTAAGTCTTATATATAAACAATTTTGGCTATTAA 229
345 TRWMMKKKARRWYWKSYACASRYKTYGWWMMKRRMSTRYCMCKWCKCKYRG 286
230 ATATGGCAACTAAGTTAGCACCCTGTAATTAGATTTTCTGGAACAATTTCTCTGAC 289
285 RRCAYTMMGRMWSYAWGKWSMCTRMYYKKGSTYMTKCTCATWYWKYWKY 226
290 TAAGAAGCTATTTGGACTGCTTTTCCCAACAAGTAGAATAAGGACCGCTCTTATAA 349
225 KRWMSKTCWSGSRGYSYTSYRSYSY-WASMMYTCMWWGRWSTWYMWAGKKWWR 167
350 AAAACCATCTCACATCGCTGGTCTGATATAAATAAAGCAATTTTATAGCTC 409
166 YATTTWRAMWMAWMTWMMYMWAMWCMSSRGAAYRRRTMMWGYRWYWKYSYRTRCA 107
410 TCGCTCTCTGCTAGTGTGTATATAAATCATTTTACCATTACCTTTTAAATAACTGT 469
106 WAYAWKTRSYWCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCW 47

QY 470 ACCTAGTTTCATCATGAGTAACTACTCAGGAGCTAAACAAAAA 513
Db 46 MMWYVYVWRAKRRMMWKRWSWSWMMWMAWGMWTRWAAARMWRW 3
RESULT 14
US-08-439-814-3
Sequence 3, Application US/08439814
Patent No. 5968735
GENERAL INFORMATION:
APPLICANT: STEIN, Ulrike
APPLICANT: WALTHER, Wolfgang
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
TITLE OF INVENTION: THERAPY-RELEVANT GENES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., Suite 330 G
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,814
FILING DATE: 12-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA: DE PCT/DE93/01086
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, Sharon N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1614-5015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B (EPO)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
FILING DATE: 10-NOV-1993
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-439-814-3

Query Match 2.0%; Score 41; DB 2; Length 1318;
Best Local Similarity 63.9%; Pred. No. 0.08;
Matches 62; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 702 ATGTTAAACATTTGTAGTAAATATTGCTAGCATTAGCTACGGAATTTTATGAAAAA 761
Db 462 ATATTAAATGTTGGCAGTATATATGGAAGGAAATTACAACTAATGTAATATGCTAAAA 521

